



SEQUENCE LISTING

<110> Junghans, Richard P.

<120> Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen

<130> 002

<140> 10/006,771

<141> 2001-12-10

<150> 60/250,090

<151> 2000-11-30

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 7654

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2428)..(3759)

<223> Chimeric IgTCR sequence contained in retroviral vector. Retroviral vector sequence (non-coding regions) are incidental to the invention. The translated (coding region) is relevant to the invention. (pertinent to Figure 3.)

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Leu Val Ala Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln															
10 15 20 25															
agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc	2550														
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr															
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Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln															
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His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp															
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Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr															
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205 210 215															
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Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly															

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Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Lys Pro Thr Thr			
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Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln			
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Pro Leu Ser Leu Arg Pro Glu Ala Ala Arg Pro Ala Ala Gly Gly Ala			
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Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly			
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Pro Arg			



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20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val  
35 40 45

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
50 55 60

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg  
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu  
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly  
115 120 125



Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Glu Val Gln  
130 135 140

Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg  
145 150 155 160

Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser  
165 170 175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile  
180 185 190

His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg  
195 200 205

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met  
210 215 220

Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu  
225 230 235 240

Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val  
245 250 255

Thr Val Ser Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro  
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu  
275 280 285

Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp  
290 295 300

Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe  
305 310 315 320

Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser  
325 330 335

Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr  
340 345 350

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys

355

360

365

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn  
 370 375 380

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu  
 385 390 395 400

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly  
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His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr  
 420 425 430

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
 435 440

&lt;210&gt; 3

&lt;211&gt; 422

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens and Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (8)..(421)

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 region (aa20-138) with leader (aal-19) (pertinent to Fig. 4A.)

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 Thr Gly Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val  
 15 20 25 30

gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc 145  
 Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe  
 35 40 45

gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa 193  
 Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys  
 50 55 60

ggt ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac 241  
 Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn  
 65 70 75

tat gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc 289

Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala  
80 85 90

aag aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc 337  
Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr  
95 100 105 110

ggg gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct 385  
Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala  
115 120 125

tat tgg ggc caa ggg acc ccg gtc acc gtc tcc tca g 422  
Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser  
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<212> PRT

<213> Homo sapiens and Mus sp.

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Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln  
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe  
35 40 45

Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala  
65 70 75 80

Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn  
85 90 95

Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val  
100 105 110

Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp  
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Gly Gln Gly Thr Pro Val Thr Val Ser Ser  
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<213> Homo sapiens and Mus sp.
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<220>
<221> CDS
<222> (14)..(712)
<223> hMN14 VLCK, humanized (CDR-grafted) anti-CEA antibody kappa light
chain V region (aa20-126), with human constant CK domain (aa127-
232) and leader (aa1-19). {pertinent to Figure 4B.)
```

aca gct aca ggt gtc cac tcc gac atc cag ctg acc cag agc cca agc 97  
Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser  
15 20 25

agt cag gat gtg ggt act tct gta gct tgg tac cag cag aag cca ggt 193  
Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly  
45 50 55 60

gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc 289  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe  
80 85 90

caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag gtg gaa atc 385  
Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile  
110 115 120

gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac 48  
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
145 150 155

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
160 165 170

caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac 577  
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
175 180 185

agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac 625  
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
190 195 200

gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc 673  
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
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Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
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Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala  
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Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val  
35 40 45

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
50 55 60

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg  
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu  
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val  
115 120 125

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
130 135 140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
145 150 155 160

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
165 170 175

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
180 185 190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
195 200 205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
210 215 220

Lys Ser Phe Asn Arg Gly Glu Cys  
225 230